

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/803,459C
Source: 1FWO
Date Processed by STIC: 1/14/05

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IFWO

RAW SEQUENCE LISTING

DATE: 01/14/2005

PATENT APPLICATION: US/10/803,459C

TIME: 12:42:13

Input Set : D:\Leptin Sequence Listing-Corrected.3.txt

Output Set: N:\CRF4\01142005\J803459C.raw

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3 <110> APPLICANT: Gertler, Arie
4      Krishna, Radha G.
6 <120> TITLE OF INVENTION: LEPTIN BINDING DOMAIN COMPOSITIONS AND METHODS THERETO
8 <130> FILE REFERENCE: 28758.1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/803,459C
C--> 10 <141> CURRENT FILING DATE: 2004-03-19
10 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: PatentIn version 3.2
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 630
16 <212> TYPE: DNA
17 <213> ORGANISM: homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)..(630)
24 <220> FEATURE:
25 <221> NAME/KEY: misc_feature
26 <222> LOCATION: (6)..(6)
27 <223> OTHER INFORMATION: n is a, c, g, or t
29 <400> SEQUENCE: 1
W--> 30 atg gcn att gat gtc aat atc aat atc tca tgt gaa act gat ggg tac      48
31 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
32 1      5      10      15
34 tta act aaa atg act tgc aga tgg tca acc agt aca atc cag tca ctt      96
35 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
36      20      25      30
38 gcg gaa agc act ttg caa ttg agg tat cat agg agc agc ctt tac tgt      144
39 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
40      35      40      45
42 tct gat att cca tct att cat ccc ata tct gag ccc aaa gat tgc tat      192
43 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
44      50      55      60
46 ttg cag agt gat ggt ttt tat gaa tgc att ttc cag cca atc ttc cta      240
47 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
48 65      70      75      80
50 tta tct ggc tac aca atg tgg att agg atc aat cac tct cta ggt tca      288
51 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
52      85      90      95
54 ctt gac tct cca cca aca tgt gtc ctt cct gat tct gtg gtg aag cca      336
55 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
56      100      105      110
58 ctg cct cca tcc agt gtg aaa gca gaa att act ata aac att gga tta      384
59 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu

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60          115          120          125
62 ttg aaa ata tct tgg gaa aag cca gtc ttt cca gag aat aac ctt caa      432
63 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
64          130          135          140
66 ttc cag att cgc tat ggt tta agt gga aaa gaa gta caa tgg aag atg      480
67 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
68 145          150          155          160
70 tat gag gtt tat gat gca aaa tca aaa tct gtc agt ctc cca gtt cca      528
71 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
72          165          170          175
74 gac ttg tgt gca gtc tat gct gtt cag gtg cgc tgt aag agg cta gat      576
75 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
76          180          185          190
78 gga ctg gga tat tgg agt aat tgg agc aat cca gcc tac aca gtt gtc      624
79 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val
80          195          200          205
82 atg gat      630
83 Met Asp
84          210
87 <210> SEQ ID NO: 2
88 <211> LENGTH: 210
89 <212> TYPE: PRT
90 <213> ORGANISM: homo sapiens
92 <400> SEQUENCE: 2
94 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr Asp Gly Tyr
95 1          5          10          15
98 Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
99          20          25          30
102 Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
103          35          40          45
106 Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
107          50          55          60
110 Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
111 65          70          75          80
114 Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
115          85          90          95
118 Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
119          100          105          110
122 Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu
123          115          120          125
126 Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
127          130          135          140
130 Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met
131 145          150          155          160
134 Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro
135          165          170          175
138 Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp
139          180          185          190
142 Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val

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143          195          200          205
146 Met Asp
147      210
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 36
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: completely synthesized
158 <400> SEQUENCE: 3
159 ggaattccat atgattgatg tcaatatcaa tatctc
162 <210> SEQ ID NO: 4
163 <211> LENGTH: 39
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: completely synthesized
170 <400> SEQUENCE: 4
171 cataggaagc tttcaatcca tgacaactgt gtaggctgg
174 <210> SEQ ID NO: 5
175 <211> LENGTH: 12
176 <212> TYPE: PRT
177 <213> ORGANISM: homo sapiens
180 <220> FEATURE:
181 <221> NAME/KEY: misc_feature
182 <222> LOCATION: (11)..(11)
183 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
185 <400> SEQUENCE: 5
W--> 187 Met Ala Ile Asp Val Asn Ile Asn Ile Ser Xaa Glu
188 1          5          10
191 <210> SEQ ID NO: 6
192 <211> LENGTH: 5
193 <212> TYPE: PRT
194 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: (3)..(3)
200 <223> OTHER INFORMATION: Consensus sequence, Xaa can be any naturally occurring amino
acid
202 <400> SEQUENCE: 6
W--> 204 Trp Ser Xaa Trp Ser
205 1          5
208 <210> SEQ ID NO: 7
209 <211> LENGTH: 627
210 <212> TYPE: DNA
211 <213> ORGANISM: gallus domesticus
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (1)..(627)
218 <220> FEATURE:

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219 <221> NAME/KEY: misc_feature
220 <222> LOCATION: (6)..(6)
221 <223> OTHER INFORMATION: n is a, c, g, or t
223 <400> SEQUENCE: 7
W--> 224 atg gcn gta gat gtg aat atc aat atc aaa tgt gaa act gat ggg tac      48
225 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
226 1          5          10          15
228 tta act aaa atg act tgc aga tgg tct gca aac cca aac gca ttg ctc      96
229 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
230          20          25          30
232 ttg ggg agt tcc ttg cag tta aga tac cac agg agc aaa att tat tgt      144
233 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
234          35          40          45
236 tct aac ttt cca agt act cct cca gaa tca gag gtg aaa gaa tgc cat      192
237 Ser Asn Phe Pro Ser Thr Pro Glu Ser Glu Val Lys Glu Cys His
238          50          55          60
240 ttc cag agg aat cat tct tat gag tgc aca ttt cag cct gtt ttt ctt      240
241 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
242 65          70          75          80
244 tta tct gga tat acc atg tgg att gag ctt aag cac tcg ctg gga aca      288
245 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
246          85          90          95
248 ctt gaa tcc tca cca act tgt gtc gtt cca gca gat gtg gtg aag cca      336
249 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
250          100          105          110
252 ctg cct ccc tcc aac att aaa gca gag atc acc aga aac gat ggg ctg      384
253 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
254          115          120          125
256 ctg aac gtg agc tgg aca aac ccc gtg ttt aca aat gat gac ctt aag      432
257 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
258          130          135          140
260 ttt cag atc cgg tac gca gtg aac agg gaa gaa ctc aca tgg gag ctg      480
261 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
262 145          150          155          160
264 tat gaa gtt cta agc gta cca aca aga tca gct gtg ata gaa gtg caa      528
265 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
266          165          170          175
268 ctt tgt gtt gaa tat att gtt cag atc cgc tgc aga gcc ctg gat ggc      576
269 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
270          180          185          190
272 tta ggc tac tgg agc aac tgg agc aga tca gcc tat gca gct gta aaa      624
273 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
274          195          200          205
276 gat      627
277 Asp
281 <210> SEQ ID NO: 8
282 <211> LENGTH: 209
283 <212> TYPE: PRT
284 <213> ORGANISM: gallus domesticus

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286 <400> SEQUENCE: 8

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288 Met Ala Val Asp Val Asn Ile Asn Ile Lys Cys Glu Thr Asp Gly Tyr
289 1          5          10          15
292 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
293          20          25          30
296 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
297          35          40          45
300 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
301          50          55          60
304 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
305 65          70          75          80
308 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
309          85          90          95
312 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
313          100         105         110
316 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
317          115         120         125
320 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
321          130         135         140
324 Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
325 145         150         155         160
328 Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
329          165         170         175
332 Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
333          180         185         190
336 Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
337          195         200         205
340 Asp

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/14/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 6

Seq#:5; Xaa Pos. 11

Seq#:6; Xaa Pos. 3

Seq#:7; N Pos. 6

VERIFICATION SUMMARY

DATE: 01/14/2005

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Input Set : D:\Leptin Sequence Listing-Corrected.3.txt

Output Set: N:\CRF4\01142005\J803459C.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0